

Result No.	Score	Query Match	Length	DB ID	Description
1	1105	100.0	212	9 US-09-817-198A-2	Sequence 2, Appli
2	1105	100.0	212	15 US-10-33-616-319 ABN	Sequence 319, App
3	1105	100.0	401	9 US-09-768-868-701 ABN	Sequence 701, App
4	1092	98.8	218	9 US-09-817-198A-5	Sequence 5, Appli
5	1077	97.5	9	US-09-817-198A-4	Sequence 4, Appli
6	832	75.3	188	9 US-09-768-868-1120	Sequence 1120, Ap
7	573	51.9	208	16 US-10-498-765A-2939	Sequence 2929, Ap
8	559	50.6	224	14 US-10-389-493-4997	Sequence 4997, Ap
9	545	49.3	213	15 US-10-276-774-2286	Sequence 2286, Ap
10	540	48.9	221	15 US-10-260-049-2465	Sequence 260, Ap
11	532	48.1	246	9 US-09-925-302-534	Sequence 534, App
12	532	48.1	246	10 US-09-922-302-534	Sequence 534, App
13	530.5	48.0	218	9 US-09-925-300-1571	Sequence 1571, App

RESULT 2

Qy 181 RMRASNELALAELBEEGKPEGPANSKTCWC 212
Db 181 RMRASNELALAELBEEGKPEGPANSKTCWC 212

US-10-362-616-319
; Sequence 319, Application US/10363616
; Publication No. US20040044181A1
; GENERAL INFORMATION:
; APPLICANT: HYSEQ, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 212-2-113 (733)
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-09-01.
; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 319
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-363-616-319

Query Match Score 100.0%; Best Local Similarity 100.0%; Matches 212;保守性 0; Mismatches 0; Indels 0; Gaps 0;

Db 61 IWDTAGQERYQTITKQYRRAGIFLYDISSERSYQHMKWVSDVDEAPEGVQKILIG 120
Qy 1 MAKYDVLFLRLLIGDSVGKTCILCRFTDNFHKSHIISTIGVDFKMKTIEVDGIKVRQ 60
Db 1 MAKYDVLFLRLLIGDSVGKTCILCRFTDNFHKSHIISTIGVDFKMKTIEVDGIKVRQ 60

Qy 61 IWDTAGQERYQTITKQYRRAGIFLYDISSERSYQHMKWVSDVDEAPEGVQKILIG 120
Db 61 IWDTAGQERYQTITKQYRRAGIFLYDISSERSYQHMKWVSDVDEAPEGVQKILIG 120
Qy 121 NKADEEQKROVGREQSQQLAKEYGMDFYETSACTNLNIKESFRTRTELVQQRKELEG 180
Db 121 NKADEEQKROVGREQSQQLAKEYGMDFYETSACTNLNIKESFRTRTELVQQRKELEG 180

Qy 181 RMRASNELALAELBEEGKPEGPANSKTCWC 212
Db 181 RMRASNELALAELBEEGKPEGPANSKTCWC 212

RESULT 3

US-09-764-868-701
; Sequence 701, Application US/09764868
; Patent No. US2002016811A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT FILING DATE: 2001-01-17
; prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SEQ ID NO 701
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-764-868-701

Query Match Score 100.0%; Best Local Similarity 100.0%; Matches 212;保守性 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MAKQYDVLFLRLLIGDSVGKTCILCRFTDNFHKSHIISTIGVDFKMKTIEVDGIKVRQ 60
Qy 27 MARQYDVLFLRLLIGDSVGKTCILCRFTDNFHKSHIISTIGVDFKMKTIEVDGIKVRQ 86

RESULT 4

US-09-817-198A-5
; Sequence 5, Application US/09817198A
; Patent No. US20030146758A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
; NUCLEAR ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
; PROTEINS, AND USES THEREOF
; FILE REFERENCE: CLO01188
; CURRENT APPLICATION NUMBER: US/09/817,198A
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 5
; SOFTWARE: FastSEQ for Windows Version 4.0

Query Match Score 1092; Best Local Similarity 97.2%; Matches 212;保守性 0; Mismatches 0; Indels 6; Gaps 1;

Db 1 MAKQYDVLFLRLLIGDSVGKTCILCRFTDNFHKSHIISTIGVDFKMKTIEVDGIKVRQ 60
Qy 61 IWDTAGQERYQTITKQYRRAGIFLYDISSERSYQHMKWVSDVDEAPEGVQKILIG 120
Db 61 IWDTAGQERYQTITKQYRRAGIFLYDISSERSYQHMKWVSDVDEAPEGVQKILIG 120
Qy 121 NKADEEQKROVGREQSQQLAKEYGMDFYETSACTNLNIKESFRTRTELVQQRKELEG 180
Db 121 NKADEEQKROVGREQSQQLAKEYGMDFYETSACTNLNIKESFRTRTELVQQRKELEG 180

Qy 175 KELEGMRMASNELALAELBEEGKPEGPANSKTCWC 212
Db 181 KELEGMRMASNELALAELBEEGKPEGPANSKTCWC 212

RESULT 5

US-09-817-198A-4
; Sequence 4, Application US/09817198A
; Patent No. US20030146758A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
; NUCLEAR ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
; PROTEINS, AND USES THEREOF
; FILE REFERENCE: CLO01188
; CURRENT APPLICATION NUMBER: US/09/817,198A
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-09-817-198A-4

Query Match Score 100.0%; Best Local Similarity 100.0%; Matches 212;保守性 0; Mismatches 0; Indels 9; Gaps 0;

Db 61 IWDTAGQERYQTITKQYRRAGIFLYDISSERSYQHMKWVSDVDEAPEGVQKILIG 120

Result No.	Score	Query	Match	Length	DB ID	Description
1	545	/cgns_6/pctodata/1/iaa/5A_COMB.pep:*	207	2	US-08-824-873-4	Sequence 4, Appli
2	545	/cgns_6/pctodata/1/iaa/5B_COMB.pep:*	207	3	US-09-198-184-4	Sequence 4, Appli
3	527.5	/cgns_6/pctodata/1/iaa/6A_COMB.pep:*	205	2	US-08-531-525-25	Sequence 25, Appli
4	527.5	/cgns_6/pctodata/1/iaa/6B_COMB.pep:*	205	2	US-08-718-270A-25	Sequence 25, Appli
5	518.5	/cgns_6/pctodata/1/iaa/6C_COMB.pep:*	198	2	US-08-531-525-51	Sequence 51, Appli
6	518.5	/cgns_6/pctodata/1/iaa/6D_COMB.pep:*	198	2	US-08-718-270A-51	Sequence 51, Appli
7	515.5	/cgns_6/pctodata/1/iaa/6E_COMB.pep:*	198	2	US-09-255-970A-12	Sequence 34, Appli
8	503.5	/cgns_6/pctodata/1/iaa/6F_COMB.pep:*	207	2	US-08-531-525-35	Sequence 35, Appli
9	503.5	/cgns_6/pctodata/1/iaa/6G_COMB.pep:*	207	2	US-08-718-270A-35	Sequence 35, Appli
10	494.5	/cgns_6/pctodata/1/iaa/6H_COMB.pep:*	198	2	US-08-531-525-10	Sequence 10, Appli
11	494.5	/cgns_6/pctodata/1/iaa/6I_COMB.pep:*	215	2	US-08-718-270A-10	Sequence 10, Appli
12	488.5	/cgns_6/pctodata/1/iaa/6J_COMB.pep:*	194	2	US-08-531-525-34	Sequence 8, Appli
13	488.5	/cgns_6/pctodata/1/iaa/6K_COMB.pep:*	194	2	US-08-718-270A-34	Sequence 34, Appli
14	478.5	/cgns_6/pctodata/1/iaa/6L_COMB.pep:*	201	2	US-08-196-901-3	Sequence 3, Appli
15	478.5	/cgns_6/pctodata/1/iaa/6M_COMB.pep:*	201	3	US-09-154-602-3	Sequence 3, Appli
16	473	/cgns_6/pctodata/1/iaa/6N_COMB.pep:*	213	4	US-09-248-796A-20293	Sequence 14, Appli
17	469	/cgns_6/pctodata/1/iaa/6O_COMB.pep:*	201	2	US-08-196-901-8	Sequence 8, Appli
18	469	/cgns_6/pctodata/1/iaa/6P_COMB.pep:*	201	3	US-09-154-602-8	Sequence 8, Appli
19	467	/cgns_6/pctodata/1/iaa/6Q_COMB.pep:*	205	4	US-09-709-103-49	Sequence 49, Appli
20	467	/cgns_6/pctodata/1/iaa/6R_COMB.pep:*	205	4	US-09-139-10A-49	Sequence 49, Appli
21	463	/cgns_6/pctodata/1/iaa/6S_COMB.pep:*	202	2	US-08-531-525-14	Sequence 14, Appli
22	463	/cgns_6/pctodata/1/iaa/6T_COMB.pep:*	202	2	US-08-718-270A-14	Sequence 14, Appli
23	462	/cgns_6/pctodata/1/iaa/6U_COMB.pep:*	227	4	US-09-248-796A-20291	Sequence 2029, Appli
24	453.5	/cgns_6/pctodata/1/iaa/6V_COMB.pep:*	201	2	US-08-531-525-13	Sequence 13, Appli
25	453.5	/cgns_6/pctodata/1/iaa/6W_COMB.pep:*	201	2	US-08-718-270A-13	Sequence 13, Appli
26	452.5	/cgns_6/pctodata/1/iaa/6X_COMB.pep:*	190	2	US-08-124-573-3	Sequence 3, Appli
27	452.5	/cgns_6/pctodata/1/iaa/6Y_COMB.pep:*	190	3	US-09-198-184-3	Sequence 3, Appli

Qy 1 MAKQDVLFRULLIGPSGVGKTCILCRAFTNEPHSSHTISTIGVDFKMKTEVDGKVKVHQ 60
 Db 1 MAKTYDLFKLILLGDSVGTCVLFRESEDAFNSTFISIIGIDKIRTELDKRIKIQ 60
 Qy 61 IWDTAGERTYOTITKQYRAQGIFLYYDDISERSYQHIMKWSVDVDETAPEGYQKILG 120
 Db 61 IWDTAGERTYOTITKQYRAQGIFLYYDDISERSYQHIMKWSVDVDETAPEGYQKILG 120
 Qy 121 NKADEFQKROVQGREQQQLAKEYGMDFYETSACTNLNKESTRTEBLVQAHRKLEGGL 180
 Db 121 NKCDYNDKROVSKERGEKLADYGIKEMTSAKANINVNAFTLARDIKAKMDKLEGN 180
 Qy 181 RMRASNE 187
 Db 181 SPOGSNQ 187

RESULT 3
 US-08-531-525-25
 ; Sequence 25, Application US/08531525
 ; Patent No. 5840683

GENERAL INFORMATION:
 / APPLICANT: Hlavka, Joseph J.
 / APPLICANT: Pincus, Matthew R.
 / APPLICANT: No. 58406831e, John F.
 / APPLICANT: Abjian, Henry B.
 / APPLICANT: Kende, Andrew S.
 / TITLE OF INVENTION: Pepides Inhibiting the Oncogenic Action
 / TITLE OF INVENTION: Pepides Inhibiting the Oncogenic Action
 / NUMBER OF SEQUENCES: 52
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Greenlee and Winner, P.C.
 / STREET: 5370 Manhattan Circle, Suite 201
 / CITY: Boulder
 / STATE: Colorado
 / COUNTRY: US
 / ZIP: 80303

COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patent Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/531,525
 / FILING DATE: 21-SEP-1995
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Ferber, Donna M.
 / REGISTRATION NUMBER: 33,878
 / REFERENCE/DOCKET NUMBER: 37-94
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (303) 499-8080
 / TELEFAX: (303) 499-8089
 / INFORMATION FOR SEQ ID NO: 25:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 205 amino acids
 / TYPE: amino acid
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 / HYPOTHETICAL: NO
 / ORIGINAL SOURCE:
 / ORGANISM: Canis familiaris
 / US-08-531-525-25

Query Match 49.3%; Score 545; DB 3; Length 207;
 Best Local Similarity 52.9%; Pred. No. 3e-52; Indels 0; Gaps 0;
 Matches 99; Conservative 45; Mismatches 43;

Qy 1 MAKQDVLFRULLIGPSGVGKTCILCRAFTNEPHSSHTISTIGVDFKMKTEVDGKVKVHQ 60
 Db 1 MAKTYDLFKLILLGDSVGTCVLFRESEDAFNSTFISIIGIDKIRTELDKRIKIQ 60
 Qy 61 IWDTAGERTYOTITKQYRAQGIFLYYDDISERSYQHIMKWSVDVDETAPEGYQKILG 120
 Db 62 DTAGQERRTTAYY-RAMGIMLVYYDTNERSFDNTRNWIRNTEEASADVEKMLG 120
 Qy 123 ADEBQKROVQGREQQQLAKEYGMDFYETSACTNLNKESTRTEBLVQAHRKLEGGL 182

Result No.	Score	Query	Match	Length	DB	ID	Description	SUMMARIES
-	-	-	-	-	-	-	-	-
1	1105	100.0	212	1	RB15_HUMAN	P59190	homo sapien	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
2	1090	98.6	212	1	RB15_MOUSE	P32289	rattus norvegicus	
3	1077	97.5	212	1	RB15_RAT	Q6di36	brachydanio	
4	872	78.9	212	2	Q6DI36	Q9lyw0	mus musculus	
5	798	72.2	168	2	Q6PA42	Q6P412	xenopus laevis	
6	686	62.1	143	2	AAH63736	Aah63736	xenopus laevis	
7	686	62.1	143	2	Q7TA34	Q7TA34	brachydanio	
8	563	55.0	200	2	Q9YTS2	Q9YTS2	caenorhabditis elegans	
9	557	50.4	211	2	BAD0734	BAD0734	bacteria	
10	546	49.5	204	2	Q15971	Q15971	drosophila melanogaster	
11	545	49.3	207	1	RB8A_CANFAM1	RB8A_CANFAM1	canis familiaris	
12	545	49.3	207	1	RB8A_HUMAN	P61006	homo sapien	
13	545	49.3	207	2	AAP35848	AAP35848	homo sapien	
14	545	49.3	207	2	QBVCF6	QBVCF6	QBvcf6 m cell line	
15	541	49.0	207	2	RAB8_DISOM	P22128	discoeye ocellaris	
16	539.5	48.8	210	1	Q6DGVS	Q6dgvs	brachydanio	
17	538.5	48.7	206	2	Q6DKL2	Q6dkl2	rattus norvegicus	
18	53.6	48.5	206	2	Q6PAW9	Q6paw9	xenopus laevis	
19	534.5	48.4	200	2	AAH60015	Aah60015	xenopus laevis	
20	534.5	48.4	203	1	RB13_HUMAN	P5153	homo sapien	
21	532	48.1	203	1	Q6GP66	Q6gp66	homo sapien	
22	532	48.1	218	2	P22127	P22127	discoeye ocellaris	
23	530.5	48.1	200	1	RB10_DISOM	P24109	canis familiaris	
24	530.5	48.0	200	1	RB10_CANFA	P61026	homo sapien	
25	530.5	48.0	200	1	RB10_HUMAN	P61027	mus musculus	
26	530.5	48.0	200	1	RB10_MOUSE	Cag33584	homo sapien	
27	530.5	48.0	200	2	CRG33584	P3586	rattus norvegicus	
28	528.5	47.8	203	1	RB13_RAT	P92330	homo sapien	
29	528.5	47.8	207	1	RB8B_HUMAN	P61028	mus musculus	
30	528.5	47.8	207	1	RB8B_MOUSE	P70550	rattus norvegicus	
31	528.5	47.8	207	2	RB8B_RAT			

ALIGNMENTS

Scoring table:	BLOSUM62
Gapop	10.0 , Gapext 0.5
Searched:	1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters:	1825181
Minimum DB seq length:	0
Maximum DB seq length:	20000000000
Post-processing: Minimum Match 0%	
Maximum Match 100%	
Listing first 45 summaries	
Database :	Uniprot_02: 1: uniprot_sprot: 2: uniprot_trembl: *
Scoring table:	BLOSUM62
Gapop	10.0 , Gapext 0.5
Run on:	December 25, 2004, 01:55:59 ; Search time 92 Seconds (without alignments) 13235.863 Million cell updates/sec
Title:	US-09-817-198C-2
Perfect score:	1105
Sequence:	1 MAKQDVLFRLLIGDSWG.....LEEEBGKPEGPANSKTCWC 212

RESULT 1						
ID	RB15_HUMAN	STANDARD	PRT;	212 AA.		
AC	P59190;	Q86TX7;	Q8TW89;			
DT	28-FEB-2003	(Rel. 41,	Created)			
DT	28-FEB-2003	(Rel. 41,	Last sequence update)			
DT	05-JUL-2004	(Rel. 44,	Last annotation update)			
DE	Ras-related protein Rab-15.					
GN	Name=RAB15;					
OS	Homo sapiens (Human)					
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo					
NCBI_TaxID	9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RA	MEDLINE=22459283;					
RA	Heilig R., Eckenberg R., Petit J.-L., Ponknecht N., Da Silva C.,					
RA	Cattolico L., Levy M., Barbe V., De Berardinis V., Urea-Vidal A.,					
RA	Pelletier B., Vico V., Arthonard V., Rowen L., Madan A., Oin S.,					
RA	Sun H., Du H., Pepin K., Artiguenave F., Robert C., Cruaud C.,					
RA	Bruel T., Jajillon O., Friedlander L., Samson G., Brotier P.,					
RA	Acire S., Segurans B., Andre F., Samain S., Crespeau H., Abbasi N.,					
RA	Aliach N., Boscu D., Dichhoff R., Dors M., Dubois I., Friedman C.,					
RA	Gouyvenoux M., James R., Madan A., Mairly-Estrada B., Ratcliffe A., Bellemere C., Belsler C., Bernard-Gonnet M.,					
RA	Bartol-Mavel D., Bourard M., Briez S., Louesse C., Lechapla C., Muselot D.,					
RA	Dufosse-Laurent V., Ferron C., Louesse C., Muselot D.,					
RA	Magdeleñat G., Pateau E., Petit E., Sirvain-Trukniewicz P., Trybou A.,					
RA	Vega-Caray N., Bataille B., Bluet E., Bordaïs I., Dubois M.,					
RA	Dumont C., Guérin T., Haefray S., Hammadi R., Muanga J., Peillouin V.,					
RA	Robert D., Wunderle B., Gauguet G., Roy A., Sainte-Marthe L.,					
RA	Verdier J., Verdier-Discala C., Hillier L.W., Fulton L., McPherson J.,					
RA	Matsuda R., Wilson R., Scarpelli C., Gygay G., Wincker P., Saurin W.,					
RA	Quetier F., Waterston R., Hood L., Weissenbach J.,					
RT	"The DNA sequence and analysis of human chromosome 14";					
RT	Nature 421:601-607 (2003).					
RN	[2]					
RP	SEQUENCE FROM N.A. (ISOFORM 2).					
RC	TISSUE:Brain.					
RA	MEDLINE=22388257;					
RA	Feingold B.A., Grouse L.H., Derge J.G.,					
RA	Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,					
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,					
RA	Jordan H., Moore T., Jordan H., Max S.J., Wang J., Hsieh F.,					
RA	Hopkins R., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,					
RA	Stepleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,					
RA	Rau B., Toshiyuki S., Casarini P., Abramson R.D., Mullany S.J.,					
RA	Boseck S.A., McEwan P.J., McKernan K.J., Malek A., Gunaratne P.H.,					
RA	Richards S., Worley K.C., Hale A.M., Gay L.J., Hulyk S.W.,					
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,					
RA	Fahy J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,					
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,					

RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimes J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.J., Skalska U., Smialius D.E., Schnerr A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	Db	61 IWDTAGQERYQTITKQYRRAGIIVFLVYDSSERSYQHIMKRVSDVDEAPEGVQKILIG 120
RA	Li W.B., Gruber C., Jesse J., Polayes D.; "Full-length cDNA libraries and normalization"; Submitted (FEB-2003) to the EMBL/GenBank/DBJ/GenBank databases.	Db	121 NKADBEQRKQVGRCIGQQQLAKEKEYGMDFETSACTNLNIKESFRTRTELVQAHRKELGL 180
CC	-!- FUNCTION: May act in concert with Rab3A in regulating aspects of synaptic vesicle membrane flow within the nerve terminal (By similarity). ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=2; Name=1; IsoId=p59190-1; Sequence=Displayed;	Db	121 NKADBEQRKQVGRCIGQQQLAKEKEYGMDFETSACTNLNIKESFRTRTELVQAHRKELGL 180
CC	Name=2; IsoId=p59190-2; Sequence=vSP_010420; Note=No experimental confirmation available;	Db	181 RMRASNELALAAELEEEGKPEGPANNSKTCWC 212
CC	-!- SIMILARITY: Belongs to the small GTPase superfamily. Rab family.	Db	181 RMRASNELALAAELEEEGKPEGPANNSKTCWC 212
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	RESULT 2	SEQUENCE FROM N.A.
CC	EMBL: BC139022; - NOT ANNOTATED_CDS.	RB15_MOUSE	RX MEDLINE:22388257; PubMed:12477932; DOI:10.1073/pnas.242603899;
CC	EMBL: BC041679; AAH40679.-.	ID	AC Q8R386;
CC	EMBL: BX48046; CAD62353.-.	DT	DT 28-FEB-2003 (Rel. 41, Created)
CC	HSSP: P32339; 1KY3	DT	DT 28-FEB-2003 (Rel. 41, Last sequence update)
CC	GeneW; HGNC:2015; RAB15.	DT	DT 05-JUL-2004 (Rel. 44, Last annotation update)
CC	InterPro: IPR003579; Gtpase_Rab.	DE	DE Ras-related protein Rab15.
CC	InterPro: IPR001806; Ras_triflrmng.	GN	GN Name=Rab15;
CC	InterPro: IPR005225; Small_GTP_P.	OS	OS Mus musculus (Mouse).
CC	Pfam: PF00071; Rab_1.	OC	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC	PRINTS: PR00449; RastransfrMNG.	OX	OX NCBI_TaxID=1090;
CC	SMART: SM00175; Rab_1.	RN	RN [1]
CC	TIGRFAMS; TIGR00231; small_GTP_1.	RP	RP SEQUENCE FROM N.A.
CC	TIGRFAMS; TIGR00231; small_GTP_1.	RX	RX MEDLINE:22388257; PubMed:12477932; DOI:10.1073/pnas.242603899;
CC	Protein transport.	RA	RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Altshul S.R., Zeeberg B., Buetow K.H., Schafer C.F., Bhat N.K., Hopkins R.F., Jordan R., Moore T., Max S.I., Wang J., Bielik F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Trapaleon M., Soares M.B., Ronald M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahay S.J., Bosak S.A., McEwan P.J.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Ketteman M., Nadan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko A., Bouffard G.G., Blakesley R.W., Touchman J.W., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., McKernan K.J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smialius D.B., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
FT	NP_BIND 15 22 GTP (By similarity).	CC	CC -!- FUNCTION: May act in concert with Rab3A in regulating aspects of synaptic vesicle membrane flow within the nerve terminal (By similarity).
FT	NP_BIND 63 67 GTP (By similarity).	CC	CC -!- SIMILARITY: Belongs to the small GTPase superfamily, Rab family.
FT	NP_BIND 121 124 S-geranylgeranyl cysteine (By similarity).	CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
FT	LIPID 210 210 S-geranylgeranyl cysteine (By similarity).	CC	CC DR EMBL: BC027769; AAH27769_1; -.
FT	LIPID 212 212 S-geranylgeranyl cysteine (By similarity).	DR	DR HSSP; P32339; 1KY3.
FT	VARSPLIC 109 212 YAPPGVQKLIGKTRALDEBQKQVGRCIGQQQLAKEKEYGMDFYE TSACTNLNIKESFRTRTELVQAHRKELGLMRASNELA ABLEEEGKPEGPANNSKTCWC -> VGDATSLPGCCEGAS PGKARRPGPKANASRKLCLPQWMKTSGTHOKASRSLLG IURMRSRGRWERSKGSSWRRSAMTSMKQVPAPTSILKSH SRV (in isoform 2).	DR	DR MGII: 191685; Rab15.
SQ	SEQUENCE 212 AA; 24390 MW; /PTid=VSP_010420.	DR	DR GO: 000515; F:protein binding; IPI: InterPro; IPR033579; GTPase_Rab.
FT	Query Match 100.0%; Score: 1.105; DB: 1; Length: 212; Best Local Similarity 100.0%; Pred. No. 7..9e-79; Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	DR Interrr; IPR01806; Ras_transfMng.
FT	1 MAQOYDVLRLILLGDSVGVKTCILLCRTDFKMTTEVDGKVKRQ 60	DR	DR Pfam: PF00071; Rab_1.
DB	1 MAQOYDVLRLILLGDSVGVKTCILLCRTDFKMTTEVDGKVKRQ 60	DR	DR SMART; SM00175; Rab_1.
Qy	61 IWDTAGQERYQTITKQYRRAGIIVFLVYDSSERSYQHIMKRVSDVDEAPEGVQKILIG 120	DR	DR TIGRFAMS; TIGR00231; small_GTP_1.
FT	GTP-binding; Lipoprotein; Prenylation; Protein transport.	FT	FT KW PT_BIND 15 22 GTP (By similarity).

Result No.	Score	Query Match Length	DB ID	Description
<hr/>				
1	1077	97.5	212	GTP-binding protein
2	559	50.6	224	hypothetical protein
3	545	49.3	207	GTP-binding protein
4	545	49.3	207	GTP-binding protein
5	532	48.1	203	GTP-binding protein
6	531.5	48.1	200	GTP-binding protein
7	530.5	48.1	200	GTP-binding protein
8	530	48.0	209	GTP-binding protein
9	526	47.6	206	GTP-binding protein
10	522.5	47.3	200	GTP-binding protein
11	519	47.0	216	GTP-binding protein
12	514	46.5	201	GTP-binding protein
13	512	46.3	216	GTP-binding protein
14	512	46.3	216	GTP-binding protein
15	510	46.2	200	GTP-binding protein
16	509	46.1	215	GTP-binding protein
17	508.5	46.0	215	GTP-binding protein
18	508	46.0	216	GTP-binding protein
19	507.5	45.9	222	GTP-binding protein
20	506	45.8	216	GTP-binding protein
21	505.5	45.7	217	GTP-binding protein
22	502.5	45.5	217	GTP-binding protein
23	501	45.3	203	GTP-binding protein
24	495.5	44.8	204	GTP-binding protein
25	492.5	44.6	215	GTP-binding protein
26	483.5	43.8	208	GTP-binding protein
27	483	43.7	208	GTP-binding protein
28	482	43.6	203	GTP-binding protein
29	480	43.4	202	GTP-binding protein

Copyright (c) 1993 - 2004 Compugen Ltd.	GenCore version 5.1.6	GRIP-binding protein
OM protein - protein search, using sw model	GRIP-binding protein	GRIP-binding protein
Run on: December 25, 2004, 05:09:38 ; Search time 78 Seconds (without alignments)	GRIP-binding protein	GRIP-binding protein
Title: US-09-817-198C-2	R;Elferink, L.A.; Arzai, K.; Scheller, R.H.	hypothetical protein
Perfect score: 1105	J. Biol. Chem. 267, 5768-5775, 1992.	GRIP-binding protein
Sequence: 1 MAKQYDVLFLILLIGDSGVG,.....LEEEBEGKPEGPANSSTKTCWC 212	A;Title: rab15, a novel low molecular weight GTP-binding protein specifically expressed in rat protein homologs; GRIP-binding protein	GRIP-binding protein
Scoring table: BLOSUM62	F;15-22/Region: nucleotide-binding motif A (P-loop)	GRIP-binding protein
Searched: Gapop 10.0 , Gapext 0.5	F;121-124/Region: GTP-binding NXXI motif F	GRIP-binding protein
Total number of hits satisfying chosen parameters: 283416	F;210-212/Region: geranyl-geranyl (Cys) (covalent)	GRIP-binding protein
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RESULT 1		
F42148		
GTP-binding protein rab15 - rat		
C;Species: Rattus norvegicus (Norway rat)		
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004		
C;Accession: F42148		
R;Elferink, L.A.; Arzai, K.; Scheller, R.H.		
J. Biol. Chem. 267, 5768-5775, 1992.		
A;Title: rab15, a novel low molecular weight GTP-binding protein specifically expressed in rat protein homologs		
A;Reference number: A42148; PMID:92210533; PMID:1313420		
A;Accession: F42148		
A;Status: preliminary		
A;Molecule type: mRNA		
A;Residues: 1-212 <ELIF>		
A;Cross-references: UNIPROT:P35289; GB:W83679; PIDN:AAA41995.1; PID:9206537		
C;Superfamily: transforming protein; translation elongation factor Tu homology		
C;Keywords: GTP binding, lipoprotein; nucleotide binding; P-loop; prenylated cysteine		
F;9-124/Domain: translation elongation factor Tu homology <ETU>		
F;15-22/Region: nucleotide-binding motif A (P-loop)		
F;210-212/Region: geranyl-geranyl (Cys) (covalent)		
ALIGNMENTS		
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Query Match Score: 97.5*		
Best Local Similarity: 97.6*		
Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;		
Qy 1 MAKQYDVLFLILLIGDSGVGKTCLLCRFTDNBPHSHIISTIGGVDFKMKTIEVDGIVKTRIQ 60		
Db 1 MAKQYDVLFLILLIGDSGVGKTCLLCRFTDNBPHSHIISTIGGVDFKMKTIEVDGIVKTRIQ 60		
Qy 61 IWDTAGBRYQTITKQYRRAGIFTYDISERSSTQHIMKRVSDVDEYAPGVQLLIG 120		
Db 61 IWDTAGBRYQTITKQYRRAGIFTYDISERSSTQHIMKRVSDVDEYAPGVQLLIG 120		
Qy 121 NKADEEQKROYGREQQOQLAKEYGMDFYETSACTNINIKESFTRLTELVLQAHRKELGL 180		
Db 121 NKADEEQKROYGREQQOQLAKEYGMDFYETSACTNINIKESFTRLTELVLQAHRKELGL 180		
Qy 181 RNCASNEALAALEEBEGKPECPANSSTKTCWC 212		
Db 181 RNCASNEALAALEEDEGKTEGPANSSTKTCWC 212		
<hr/>		
RESULT 2		
T3855		
hypothetical protein D1037.4 - Caenorhabditis elegans		
C;Species: Caenorhabditis elegans		
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 11-Jan-2000		
C;Accession: T3855		
R;Bedwith, J.; Biewald, T.		
submitted to the EMBL Data Library, November 1998		
A;Description: The sequence of C. elegans cosmid D1037.		

A;Reference number: 221424	Qy 61 IWDTAGQERYQTITKQYRRAQGILVYDIDSSERSYQHIMKWKVSDVDEYAPEGVQKILIG 120
A;Accession: T33855	Db 61 IWDTAGQERYQTITKQYRRAQGILVYDIDSSERSYQHIMKWKVSDVDEYAPEGVQKILIG 120
A;Status: preliminary	C;Species: Canis lupus familiaris (dog)
A;Molecule type: DNA	C;Accession: B36164; S15604
A;Residues: 1-224 <LFB>	C;Title: 28-Mar-1991 #sequence_change 09-Jul-2004
A;Cross-references: EMBL:AF106592; PIDN:AC78494_1; GSPDB:GN00019; CESP:D1037_4	R;Chavrier, P.; Vingron, M.; Sander, C.; Simons, K.; Zesail, M.
A;Experimental source: strain Bristol N2; clone D1037	Mol. Cell. Biol. 10, 6578-6585, 1990
C;Generics:	A;Title: Molecular cloning of YPT1 SEC4-related cDNAs from an epithelial cell line.
A;Gene: CESP:D1037_4	A;Reference number: A36364; MUID:91061765; PMID:2123294
A;Map Position: 1	A;Status: preliminary
A;Introns: 10/3; 62/2; 82/3; 181/1	A;Molecule type: mRNA
C;Superfamily: ras transforming protein; translation elongation factor Tu homology	A;Residues: 1-207 <CHA>
Query Match 50.6%; Score 559; DB 2; Length 224;	A;Cross-references: UNIPROT:P61007; GB:X56385; NID:g920; PIDN:CA56776_1; PMID:9606436
Best Local Similarity 55.3%; Pred. No. 2.2e-37;	C;Superfamily: ras transforming protein; translation elongation factor Tu homology
Matches 105; Conservative 42; Mismatches 39; Indels 4; Gaps 1;	R;Keywords: GTP binding; lipoprotein; membrane trafficking; nucleotide binding; P-loop; ETU>
RESULT 4	F;15-22/Region: nucleotide-binding motif A (p-loop)
Qy 1 MAKQDYVLFRILLGIDSGVGKTCILCRFTDNEPHSASHISITIGVDGIVKVRIO 60	F;121-124/Region: GTP-binding NKX motif F
Db 1 MARTYDYLFKLILLGIDSGVGKTCILCRFTDNEPHSASHISITIGVDGIVKVRIO 60	F;151-153/Region: GTP-binding SAK/L motif F
Qy 61 IWDTAGQERYQTITKQYRRAQGILVYDIDSSERSYQHIMKWKVSDVDEYAPEGVQKILIG 120	F;204/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
Db 61 IWDTAGQERYQTITKQYRRAQGILVYDIDSSERSYQHIMKWKVSDVDEYAPEGVQKILIG 120	Query Match 49.3%; Score 545; DB 2; Length 207;
Qy 121 NKADEEQKRVQGREQQQLAKEKEYSFRTRTELYQAHRKELFGL 180	Best Local Similarity 52.9%; Pred. No. 2.6e-36;
Db 121 NKCDEERREYSRDRGEQIALEYGKFLIEISAKANLNIDEAFFTLARDI----RSKRMQN 176	Matches 99; Conservative 45; Mismatches 43; Indels 0; Gaps 0;
Qy 181 RMRASNELAI 190	Qy 1 MAKQYVNLFRALLGIGSGVGTICLICRFTDNEPHSASHISITIGVDGIVKVRIO 60
Db 177 EMRAATGAIA 186	Db 1 MARTYDYLFLKLLIGSGVGKTCILCRFTDNEPHSASHISITIGVDGIVKVRIO 60
RESULT 3	Qy 61 IWDTAGQERYQTITKQYRRAQGILVYDIDSSERSYQHIMKWKVSDVDEYAPEGVQKILIG 120
B49647 GTP-binding protein rab8 - human	Db 61 IWDTAGQERYQTITKQYRRAQGILVYDIDSSERSYQHIMKWKVSDVDEYAPEGVQKILIG 120
C;Species: Homo sapiens (man)	C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004	C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
R;Zahraoui, A.; Arpin, M.; Fontaine, J.J.; Hellio, R.; Tavitian, A.; Louvard, J. Cell Biol. 124, 101-115, 1994	R;Zahraoui, A.; Arpin, M.; Fontaine, J.J.; Hellio, R.; Tavitian, A.; Louvard, J. Cell Biol. 124, 101-115, 1994
A;Title: A small rab GProtein is distributed in cytoplasmic vesicles in non polarized cell	A;Title: Isoprenylation of rab proteins possessing a C-terminal CaaX motif.
A;Reference number: A43647; MUID:94124602; PMID:8294494	A;Reference number: S36817; MUID:93387463; PMID:837553
A;Accession: B49647	A;Status: preliminary
A;Molecule type: mRNA	A;Residues: 175-186 <CDB>
A;Residues: 1-207 <ZAH>	C;Superfamily: GTP-binding protein; translation elongation factor Tu homology
A;Cross-references: UNIPROT:P61006; EMBL:X56741; NID:9452317; PIDN:CAA40065_1; PMID:94523	C;Keywords: GTP binding; lipoprotein; membrane trafficking; nucleotide binding; P-loop
FEBS Lett. 310, 323-328, 1993	F;15-22/Region: nucleotide-binding motif A (p-loop)
R;Obreitter, G.; Tavitian, A.; Zahraoui, A.	F;121-124/Region: GTP-binding NKX motif F
A;Title: Isoprenylation of rab proteins possessing a C-terminal CaaX motif.	F;151-153/Region: GTP-binding SAK/L motif F
A;Reference number: S36817; MUID:93387463; PMID:837553	F;204/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
A;Status: preliminary	Query Match 49.3%; Score 545; DB 2; Length 207;
A;Molecule type: mRNA	Best Local Similarity 52.9%; Pred. No. 2.6e-36;
C;Superfamily: ras transforming protein; translation elongation factor Tu homology	Matches 99; Conservative 45; Mismatches 43; Indels 0; Gaps 0;
C;Keywords: GTP binding; lipoprotein; membrane trafficking; nucleotide binding; P-loop	Qy 1 MAKQYVNLFRALLGIGSGVGTICLICRFTDNEPHSASHISITIGVDGIVKVRIO 60
F;15-22/Region: nucleotide-binding motif A (p-loop)	Db 1 MARTYDYLFLKLLIGSGVGKTCILCRFTDNEPHSASHISITIGVDGIVKVRIO 60
F;121-124/Region: GTP-binding NKX motif F	C;Species: Homo sapiens (man)
F;151-153/Region: GTP-binding SAK/L motif F	C;Accession: A49647
F;204/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted	R;Zahraoui, A.; Oberty, G.; Arpin, M.; Fontaine, J.J.; Hellio, R.; Tavitian, A.; Louvard, J. Cell Biol. 124, 101-115, 1994
Query Match 49.3%; Score 545; DB 2; Length 207;	A;Title: A small rab GProtein is distributed in cytoplasmic vesicles in non polarized cell
Best Local Similarity 52.9%; Pred. No. 2.6e-36;	A;Reference number: A43647; MUID:94124602; PMID:8294494
Matches 99; Conservative 45; Mismatches 43; Indels 0; Gaps 0;	A;Status: preliminary
Qy 1 MAKQYVNLFRALLGIGSGVGTICLICRFTDNEPHSASHISITIGVDGIVKVRIO 60	A;Molecule type: mRNA
Db 1 MARTYDYLFLKLLIGSGVGKTCILCRFTDNEPHSASHISITIGVDGIVKVRIO 60	A;Cross-references: UNIPROT:P51153; EMBL:X75593; NID:9452319; PIDN:CAA53266_1; PMID:94523;
C;Superfamily: ras transforming protein; translation elongation factor Tu homology	C;Superfamily: Homo sapiens (man)

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OM protein - protein search, using SW model

Run on: December 25, 2004, 01:51:44 ; Search time 308 Seconds
(without alignments)

246.918 Million cell updates/sec

Title: US-09-817-198C-2

Perfect score: 1105

Sequence: 1 MAKQYDVLFLRLLIGDSGVG.....LEEEEGKPEGPANSSTKTCWC 212

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 35872999 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: geneseqD1980s:*
- 2: geneseqD1990s:*
- 3: geneseqD2000s:*
- 4: geneseqD2001s:*
- 5: geneseqD2002s:*
- 6: geneseqD2003as:*
- 7: geneseqD2003bs:*
- 8: geneseqD2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	1105	100.0	212	5 ABP62882	Abp62882 Human pol
2	1105	100.0	212	6 AAe29096	Aae29096 Human Ras
3	1105	100.0	401	4 AAU17136	AAU17136 Novel sig
4	1105	100.0	401	7 ADB93844	ADB93844 Human nov
5	1092	98.8	218	3 AAB41604	AAB41604 Human ORF
6	1077	97.5	212	7 ADB58127	ADB58127 Rat Prote
7	832	75.3	188	4 AAU17555	AAU17555 Novel sig
8	832	75.3	188	7 ADB94263	ADB94263 Human nov
9	573	51.9	208	7 ADT71123	ADT71123 Human hea
10	546.5	49.5	204	4 ABP70670	ABP70670 Drosophil
11	545	49.3	207	7 ADB58121	ADB58121 Human Pro
12	545	49.3	213	4 ABB11916	ABB11916 Human rab
13	540	48.9	221	5 ABP41333	ABP41333 Human ova
14	532	48.1	203	7 ADB83429	ADB83429 Human Pro
15	532	48.1	203	7 ADB58125	ADB58125 Human Pro
16	532	48.1	246	3 AAB8196	AAB8196 Lung canc
17	530.5	48.0	200	3 AAB09797	AAB09797 Human Rab
18	530.5	48.0	200	3 AAU19165	AAU19165 Amino aci
19	530.5	48.0	200	4 AAB95340	AAB95340 Human pro
20	530.5	48.0	200	8 ADN05082	ADN05082 Antipsoni
21	528.5	48.0	218	3 AAB56993	AAB56993 Human pro
22	529.5	47.9	218	4 ABG07266	ABG07266 Novel hum
23	528.5	47.8	207	4 ABB71647	ABB71647 Drosophil
24	528.5	47.8	207	4 AA667154	AA667154 Amino aci
25	528.5	47.8	207	4 AAB92628	AAB92628 Human pro

ALIGNMENTS

26	528.5	47.8	207	5 ABP65204	ABP65204 Hypoxia-r
27	528.5	47.8	207	8 ADH68266	ADH68266 Human G-P
28	526.5	47.6	200	7 ADI69495	ADI69495 Human hea
29	526	47.6	201	3 AAB09982	AAB09982 Canine Ra
30	523	47.3	199	3 AAB09980	AAB09980 Human Rab
31	523	47.3	199	3 AAB09981	AAB09981 Human Rab
32	523	47.3	206	6 ABJ26542	ABJ26542 Aspergill
33	523	47.3	206	6 ABJ25583	ABJ25583 Aspergill
34	519	47.0	216	3 AAC53945	AAC53945 Arabidops
35	519	47.0	216	3 AAC08688	AAC08688 Arabidops
36	519	47.0	253	3 AAC53944	AAC53944 Arabidops
37	519	47.0	254	3 AAC08687	AAC08687 Arabidops
38	514	46.5	201	6 AAO19956	AAO19956 C elegans
39	513.5	46.5	215	6 AAC026373	AAC026373 Zea mays
40	512	46.3	190	6 AAC026373	AAC026373 Ras-like
41	512	46.3	216	8 ADN72851	ADN72851 Thale cre
42	510	46.2	218	3 AAC19220	AAC19220 Arabidops
43	507	45.9	216	3 AAC08006	AAC08006 Arabidops
44	506.5	45.8	209	4 ABG23335	ABG23335 Novel hum
45	501	45.3	224	3 AAC47826	AAC47826 Arabidops

RESULT 1

ABP62882 standard; protein; 212 AA.

ABP62882;

XX DT 14-OCT-2002 (first entry)

XX DE Human polypeptide SEQ ID NO 319.

XX KW Human; vulnary; dermatological; neuroprotective; nootropic; cancer;

KW antiparkinsonian; immunostimulant; cytostatic; immunosuppressive;

KW antidiabetic; antiallergic; gene therapy; wound healing; tissue repair;

KW central nervous system disorder; Alzheimer's disease;

KW Parkinson's disease; Huntington's disease; immune disorder;

KW autoimmune disorder; multiple sclerosis; diabetes; allergy.

Homo sapiens.

WO200218424-A2.

XX PN XX

XX PD 07-MAR-2002.

XX PR 31-AUG-2001; 2001WO-US0227093.

XX PR 01-SEP-2000; 2000US-00654935.

XX (HYSEQ INC.

XX PA Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;

PI PI Zhao QA, Wang D, Liu C, Drmanac RT, Wehrman T;

XX XX WPI: 2002-583321/62.

DR N-PSDB; AB093361.

XX

PT New polynucleotide and polypeptides, useful for treatment and diagnosis

PT of Alzheimer's, Parkinson's, Huntington's, amyotrophic lateral

PT sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple

PT allergies.

PS Claim 20; SEQ ID NO 319; 284pp + Sequence Listing; English.

XX

CC The invention relates to an isolated polynucleotide (I) comprising one of

CC sequences (ABQ9288-BQ93332). Treating a condition comprising

CC 245 sequences of Alzheimer's, Parkinson's, Huntington's, amyotrophic lateral

CC sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple

CC allergies.

XX

CC The invention relates to a composition comprising the protein

CC (II) encoded by (I) (ABP6280-ABP6053) or an antibody (III) to (II).

CC (I), (II) and (III) are useful for diagnostic evaluation of disorders.

CC (I) is useful for gene therapy of diseases and (II) can be used for

CC

CC	therapeutic treatment. Diseases that may be treated include wound healing and tissue repair, burns, central nervous system disorders (e.g.	FT	/note= "Protein kinase C phosphorylation site"
CC	Alzheimer's, Parkinson's, Huntington's and amyotrophic lateral	XX	WC0200277193-A2.
CC	sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple	PN	
CC	sclerosis, diabetes and allergies. Note: The sequence data for this	XX	03-OCT-2002.
CC	patent did not form part of the printed specification, but was obtained	PD	
CC	in electronic format directly from WIPO at	XX	27-MAR-2002; 2002WO-US009328.
CC	ftp.wipo.int/pub/published_pct_sequences	XX	
XX	Sequence 212 AA:	PR	27-MAR-2001; 2001US-00817198.
SQ			

Query	Match	Score	Length	DB	ID	RESULT
Query	Match	100.0%	Score 1105;	DB 5;		2
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Db	1	MAKQDVLFVRLLLGDSVGKTCILCREFDNEPHSSHTISTIGVDPKMKTIEVDGKVRIQ	60			
Qy	61	IWDTAGQERYQTITKQQYTRRAQGFLYYDISSERSYQHIMKRVSDYEAPGVKILIG	120			
Db	61	IWDTAGQERYQTITKQQYTRRAQGFLYYDISSERSYQHIMKRVSDYEAPGVKILIG	120			
Qy	121	NKADEEQKRQVGHQEGQQLAKEYGMDFYETSACTNIKESTRTLTELVLQAHRKELEG	180			
Db	121	NKADEEQKRQVGHQEGQQLAKEYGMDFYETSACTNIKESTRTLTELVLQAHRKELEG	180			
Qy	181	RMRASNEALAALEEEBKEKPEGPANSKTCWC	212			
Db	181	RMRASNEALAALEEEBKEKPEGPANSKTCWC	212			
				AAE29096	AAE29096	standard; protein; 212 AA.
				AAE29096	AAE29096	

Human Ras-like protein. Human; Ras-like protein; inflammation; cell proliferation; apoptosis; immunodeficiency; neurodegenerative; Alzheimer's disease; cirrhosis; Parkinson's disease; wasting disease; Cachexia; myocardial infarction; osteoporosis; atherosclerosis; glomerulonephritis; Crohn's disease; irritable bowel syndrome; multiple sclerosis; sarcoidosis; Pancratitis; autoimmune thyroiditis; osteoarthritis; allergy; Sjogren's syndrome; infection; transgenic; gene therapy; nootropic; gout; neuroprotective; vasotropin; cytosolic; dermatological; nephrotropic; ophthalmological; tranquiliser; cancer; stroke; Grave's disease; AIDS; asthma; anaemia; drug screening.

Homo sapiens.	
Key	Location/Qualifiers
TH	15. .22
Binding-site	/note= "ATP/GTP binding site motif A"
TT	18. .23
Modified-site	/note= "N-myristoylation site"
TT	.29. .32
Modified-site	/note= "Casein kinase II phosphorylation site"
TT	.92. .94
Modified-site	/note= "Protein kinase C phosphorylation site"
TT	.101. .109
Modified-site	/note= "Tyrosine kinase phosphorylation site"
TT	.104. .107
Modified-site	/note= "casein kinase II phosphorylation site"
TT	.136. .141
Modified-site	/note= "N-myristoylation site"
TT	.205. .208
Modified-site	/note= "N-glycosylation site"
TT	.206. .208

RESULT 3
AAU17136 ID AAU17136 Standard: protein: 401 AA

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OM nucleic - nucleic search, using sw model

Run on: December 24, 2004, 23:12:29 ; Search time 1599 Seconds
(without alignments)
11341.838 Million cell updates/sec

Title: US-09-817-198C-1

Perfect score: 3257

Sequence: 1 tgccgcgtgccggcgccg.....aaaaaaa.....aaaaaaa 3257

Scoring table: IDENTITY_NUC Gapext 1.0

Searched: 4105333 seqs, 2784095677 residues

Total number of hits satisfying chosen parameters: 82106666

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:^{*}

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 2: /cn2_6_ptodata/2_pubpna/pctu_NEW_PUB.seq:
 3: /cn2_6_ptodata/2_pubpna/pctu_NEW_PUB.seq:
 4: /cn2_6_ptodata/2_pubpna/pctu_NEW_PUB.seq:
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 7: /cn2_6_ptodata/2_pubpna/us08_PUCOMB.seq:
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 10: /cn2_6_ptodata/2_pubpna/us09C_PUCOMB.seq:
 11: /cn2_6_ptodata/2_pubpna/us09_NEW_PUB.seq:
 12: /cn2_6_ptodata/2_pubpna/us10_PUCOMB.seq:
 13: /cn2_6_ptodata/2_pubpna/us10A_PUCOMB.seq:
 14: /cn2_6_ptodata/2_pubpna/us10B_PUCOMB.seq:
 15: /cn2_6_ptodata/2_pubpna/us10C_PUCOMB.seq:
 16: /cn2_6_ptodata/2_pubpna/us10D_PUCOMB.seq:
 17: /cn2_6_ptodata/2_pubpna/us10E_PUCOMB.seq:
 18: /cn2_6_ptodata/2_pubpna/us10_NEW_PUB.seq:
 19: /cn2_6_ptodata/2_pubpna/us11_NEW_PUB.seq:
 20: /cn2_6_ptodata/2_pubpna/us60_NEW_PUB.seq:
 21: /cn2_6_ptodata/2_pubpna/us60_PUCOMB.seq:

RESULT 1

US-09-817-198A-1

; Sequence 1, Application US/09817198A
 ; Patent No. US2004146755A1
 ; GENERAL INFORMATION:
 ; APPLICANT: YE, Jane et al.
 ; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS, NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE PROTEINS, AND USES THEREOF
 ; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
 ; FILE REFERENCE: CL001188
 ; CURRENT APPLICATION NUMBER: US/09-817,198A
 ; CURRENT FILING DATE: 2001-03-27
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 3257
 ; TYPE: DNA
 ; ORGANISM: Human
 US-09-817-198A-1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3257	100.0	3257	9 US-09-817-198A-1	Sequence 1, Appli
2	2696.6	82.8	28770	9 US-09-817-198A-3	Sequence 3, Appli
3	1192.8	36.6	7924	15 US-10-511-455-2111	Sequence 211, Ap
4	1192.8	36.6	7924	16 US-10-511-455-2111	Sequence 151, App
C	6 1160.8	35.6	7924	15 US-10-511-455-2112	Sequence 211, Ap
C	7 1160.8	35.6	2021	9 US-09-764-868-88	Sequence 152, App
8	1000.2	30.7	1054	16 US-10-363-616-74	Sequence 74, Appli
9	599	18.4	601	9 US-09-817-198A-28	Sequence 28, Appli
10	599	18.4	601	9 US-09-817-198A-29	Sequence 29, Appli
11	595	17.5	594	15 US-10-049-388-7810	Sequence 7830, Ap
12	540	16.6	601	9 US-09-817-198A-30	Sequence 30, Appli

Query Match	Best Local Similarity	Score	DB	Length	SEQ ID NO
1	100.0%	3257	9	3257	1
2	100.0%	3257	9	3257	1
3	100.0%	3257	9	3257	1
4	100.0%	3257	9	3257	1
5	100.0%	3257	9	3257	1
6	100.0%	3257	9	3257	1
7	100.0%	3257	9	3257	1
8	100.0%	3257	9	3257	1
9	100.0%	3257	9	3257	1
10	100.0%	3257	9	3257	1
11	100.0%	3257	9	3257	1
12	100.0%	3257	9	3257	1

181	AGATGAAGACCATAGGTTAGCGGATCAAGTCCGATACAGATCTGGGACACTGCCG	240	Qy
181	AGATGAAGACCATAGGTTAGCGGATCAAGTCCGATACAGATCTGGGACACTGCCG	240	b
241	GGCAGGAGAGATAACGACCATCACAAAGGAGTACTATTCGCGGCCCCAGGGATATT	300	b
241	GGCAGGAGAGATAACGACCATCACAAAGGAGTACTATTCGCGGCCCCAGGGATATT	300	b
301	TGGTCTATGCAATTAGCGGAGGGCTCTTACCGACATCATGAAAGTGGCTAGTGACG	360	y
301	TGGTCTATGCAATTAGCGGAGGGCTCTTACCGACATCATGAAAGTGGCTAGTGACG	360	b
421	AGCGAAGAAGGGCAGTGGCAAGAGCAGGGCAGTGGCAAGAGTATGGATGG	480	y
421	AGCGAAGAAGGGCAGTGGCAAGAGCAGGGCAGTGGCAAGAGTATGGATGG	480	b
481	ACTCTATGAAACAGTGGCTGACCAACTCAACATTAAGAGTCATTCAACCGTCTGA	540	y
481	ACTCTATGAAACAGTGGCTGACCAACTCAACATTAAGAGTCATTCAACCGTCTGA	540	b
541	ATGAGCTGETGTCGAGAGCTGGCAAGGCGCTCGGATGGCTGGCCAGCA	600	y
541	ATGAGCTGETGTCGAGAGCTGGCAAGGCGCTCGGATGGCTGGCCAGCA	600	b
601	CAGAGCTGCACTGGCAAGAGCTGGCAAGGCGCTCGGATGGCTGGCCAGCA	660	y
601	CAGAGCTGCACTGGCAAGGCGCTCGGATGGCTGGCCAGCA	660	b
661	CTTCGAAAACACTCTGGGAGGAGCTGGCAAGGCGCTCGGATGGCTGGCCAGCA	720	y
661	CTTCGAAAACACTCTGGGAGGAGCTGGCAAGGCGCTCGGATGGCTGGCCAGCA	720	b
721	CTTCGAGGCCCCTGGGAGAAGGGAGGCCAACCGAGGGCCAGCGAAC	780	y
721	CTTCGAGGCCCCTGGGAGAAGGGAGGCCAACCGAGGGCCAGCGAAC	780	b
781	GTTGATGACCTATTGATGATCAGTAGCCACTACTCCCCCTGCTGGCTGGGG	840	y
781	GTTGATGACCTATTGATGATCAGTAGCCACTACTCCCCCTGCTGGCTGGGG	840	b
841	CTGCTGTCACTCTCAAGGAGCCCTGTGCCCAAGGCCCTGCTGGCTCTCTCA	900	y
841	CTGCTGTCACTCTCAAGGAGCCCTGTGCCCAAGGCCCTGCTGGCTCTCTCA	900	b
901	GCCTGTTTCCCAAGGCCAACGGGCTGTGCTGAGCCCAACACTGTCTC	960	y
901	GCCTGTTTCCCAAGGCCAACGGGCTGTGCTGAGCCCAACACTGTCTC	960	b
961	ACCATCCGCCACCAAGAACACCCACCAAGGCCAACACTGTCTC	1020	y
961	ACCATCCGCCACCAAGAACACCCACCAAGGCCAACACTGTCTC	1020	b
1081	TGACCCCTCCCTCCCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1140	y
1081	TGACCCCTCCCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1140	b
1141	CCTGCTGTGTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1200	y
1141	CCTGCTGTGTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1200	b
1201	GCTCTGGGAGGGTTCACCCCTGATCCAGGAGAACCCCTACCCCTGCTGCTG	1260	y
1201	GCTCTGGGAGGGTTCACCCCTGATCCAGGAGAACCCCTACCCCTGCTGCTG	1260	b
2341	CITCATATGTAAGGATAAGAACCTCACTCCCTACTCTCCAAAAGAGTGGGAAAGA	2400	Qy

Result No.	Score	Query Match Length	DB ID	Description
1	202.6	6.2	412	Sequence 1698, Ap
2	174.5	5.3	730	Sequence 16, App1
3	159.2	4.9	1799	Sequence 36, App1
4	156.6	4.8	1340	Sequence 2, App1
5	156.6	4.8	1340	Sequence 2, App1
6	156	4.8	925	Sequence 4, App1
7	156	4.8	925	Sequence 4, App1
8	145.2	4.5	875	Sequence 1782, Ap
9	144.6	4.4	3936	Sequence 49, App1
10	141	4.3	2552	Sequence 15247, A
11	139	4.3	1053	Sequence 12052, A
12	138	4.2	842	Sequence 6, App1
13	137	4.2	282	Sequence 2183, Ap
14	136.2	4.2	875	Sequence 10, App1
15	136.2	4.2	1106	Sequence 959, App1
16	136.2	4.2	2612	Sequence 142, App1
17	133.4	4.1	1069	Sequence 646, App1
18	133	4.1	135	Sequence 16632, A
19	127.2	3.9	1090	Sequence 914, App1
20	124.2	3.8	723	Sequence 1422, Ap
21	123.6	3.8	1102	Sequence 828, App1
22	122.6	3.8	8137	Sequence 142, App1
23	120.6	3.7	847	Sequence 4, App1
24	119.6	3.7	684	Sequence 6188, App1
25	118.4	3.6	928	Sequence 1443, A
26	118	3.6	645	Sequence 1383, App1
27	118	3.6	645	Sequence 16665, A

Qy 257 GACCATCACAAACGAGTACTATGGCGGCCAGGGATAATTGGCTATGACATTAG 316
 Db 241 GAGATCACAAGCCCTACTAAGGGTGCAGTGGATGACATAC 300
 Qy 317 CAGCGAGGCTTCATCCAGCACATCATGAATGGGTCAGTGACGGCACC 376
 Db 301 CAAAGGAGAAGTCTTCGAAACATCCGAACATGGAACTGGACCCCTC 360
 Qy 377 AGAGGGCTCCAGAAGATCCTATTGGAAATAGGTCTATAGGGCAGA 427
 Db 361 TGAGACCTCGAAAGATGATACTYGGAACAGTGATGATGAAACA 411
 Qy 607 TGG 609
 Db 641 TGG 643

RESULT 2
 US-09-300-958A-16
 Sequence 16, Application US/09300958A
 / Patent No. 6435319
 / GENERAL INFORMATION:
 / APPLICANT: McClelland, Michael
 / APPLICANT: Welsh, John
 / APPLICANT: Trinkle, Thomas
 / TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
 / FILE REFERENCE: P-PH 3457
 / CURRENT APPLICATION NUMBER: US/09/300, 958A
 / PRIOR APPLICATION NUMBER: 60/083, 331
 / PRIOR FILING DATE: 1998-04-27
 / PRIOR APPLICATION NUMBER: 60/098, 070
 / PRIOR FILING DATE: 1998-08-27
 / PRIOR APPLICATION NUMBER: 60/118, 624
 / PRIOR FILING DATE: 1999-02-04
 / NUMBER OF SEQ ID NOS: 85
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO: 16
 / LENGTH: 730
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / FILE REFERENCE: US-09-300-958A-16

Query Match Score 174.2; DB 4; Length 730;
 Best Local Similarity 5.3%; Pred. No. 2.5e-37;
 Matches 342; Conservative 0; Mismatches 258; Indels 3; Gaps 1;

Qy 7 CTGCCGCGCCGAGTTCCCGCCCGTGGCCAGTCTGGCAAGAGTAGATTCG 66
 Db 44 CGAACCCGCCGCCGCCGGCTCGCCCGCCATGGCCGGAACTAGGACAC 103
 Qy 67 TGTTCGGCTGCTGCTGATGGGAACTCCGGGTTGGCAAGA CCTGGCTGCTG 126
 Db 104 TCTTAAGGTGCTCATCATGGGACAGGGTGTGGCAAGGAGTTACTGGGT 163
 Qy 127 TAACGGACAGAGTTCCACTCTGGACATCTGGGAACTCGGGTGA 186
 Db 164 TTGAGACACACTTCTAGGAGCTAACATCCACATGGATGATCAGATTC 223
 Qy 187 AGACCATAGAGGTGACGGCATCAAAGTGGGAACTCGGGTGA 246
 Db 224 GGACGTGGAGTAACGGGAGAGGGCTAACAGCATGGACATCTGGACAGGGCAGG 283
 Qy 247 AGAGATACCAGACCATCAAAGCAGTACTGGGGAACTTGGGATATTGGCT 306
 Db 284 AGCGCTTCGGACCATCACCTCCAGPATATGGGGACCCACGGGTCACTGGTT 343
 Qy 307 ATGACATAGCAGGGAGCTAACAGCATGGGAACTGGGATAGGTGGATG 366
 Db 344 ACAGACGTCAACCTGGCACTTGTGCAACTGTCAGGGTGGGTTCAAGAAC 403
 Qy 367 ATGACGACAGAGGGCTCCAGAAGATCCTATTGGGATAAGGCTGATGAGGACAGA 426
 Db 404 AGAC--TGTGATGAGTGTGGCAATTAGTGGGATAAGAATGACACCTGGAC 460
 Qy 427 AACGGCACGGGGAAAGAGCAAGGCCAGCTGGGAAGGGAGTATGGCATGGACTCT 486

Db 461 GGAAAGGTGGAGAACGGAGATGGCTCATGGGCAATGGCATCCAGTC 520
 Qy 487 ATGAAACAAGTGGCTGACCAACCTCAACATAAGAGTCATTCAGAGGC 546
 Db 521 TCGAACCCAGGGCAAGGGAATCTCAACTGTCATCAGGGGC 580
 Qy 547 TGGCTGTGGCCCATGGAAAGGCTGGATGGCTGGAAATGAGT 605
 Db 581 TGGCTCTGGAGAACCTGGCAAAGAGAACAGGAGCTGGAAACAGGATG 640

Db 607 TGG 609
 Qy 641 TGG 643

RESULT 3
 US-09-774-528-36
 / Sequence 36, Application US/09774528
 / Patent No. 6741619
 / GENERAL INFORMATION:
 / APPLICANT: Tang, Y. Tom
 / APPLICANT: Zhou, Ping
 / APPLICANT: Goodrich, Ryle
 / APPLICANT: Liu, Chenghua
 / APPLICANT: Asundi, Vinod
 / APPLICANT: Ren, Feiyan
 / APPLICANT: Zhang, Jie
 / APPLICANT: Zhao, Qing A.
 / APPLICANT: Yang, Yonghong
 / APPLICANT: Xue, Aidong J.
 / APPLICANT: Wehrman, Tom
 / APPLICANT: Wang, Jian-Rui
 / APPLICANT: Wang, Dunrui
 / APPLICANT: Drmanac, Radoje T.
 / TITLE OF INVENTION: No. 6743619el Nucleic Acids and
 / TITLE OF INVENTION: Polypeptides
 / FILE REFERENCE: 802
 / CURRENT APPLICATION NUMBER: US/09/774, 528
 / CURRENT FILING DATE: 2001-01-30
 / NUMBER OF SEQ ID NOS: 441
 / SOFTWARE: PT_FL_genes Version 2.0
 / SEQ ID NO: 36
 / LENGTH: 1799
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / FEATURE: CDS
 / NAME/KEY: CDS
 / LOCATION: (124) .. (831)
 / FILE REFERENCE: US-09-774-528-36

Query Match Score 159.2; DB 4;
 Best Local Similarity 59.5%; Pred. No. 5.4e-33;
 Matches 288; Conservative 0; Mismatches 193; Indels 3; Gaps 1;

Qy 49 CGAAGGAGTAGCTGGCTGCTTCCGGCTGCTGGGACTCTGGGATCTGGCTGATCGGGGAAAGA 108
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 Qy 109 CCTGCTGCTGCTGGCTTACGGAAACGGTTCACTCTTCGCACTTCACATGGCTGATGGCTG 168
 Db 263 CCAGCTGTGATGGGGCTTACCGGAGACACCTTCTGGAGGCTGCACTGGCTG 322
 Qy 169 GTGTTGACTTTAAGTGAAGGACATAGGGCTAACGGGATCAAGTGGGATCTGGCTG 228
 Db 323 GTGTTGACTTCATCAATCAACATGTAAGGAAATATGGATTACAGATT 382
 Qy 229 GGGACATCTGGAGGGGAGGAGATAACAGGAGCTACATGGGGGCC 288
 Db 383 GGAAACAGGAGGTGGGAGATTCAGCTAACAGGAACTTACAGAGGTGCCA 442
 Qy 289 AGGGGATATTTTGGCTATGACATTAGGAGGCTCTTACAGGACATCATGAGT 348

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4	883.4	27.1	955	5	BX397021 BX397021
5	856	26.3	957	5	BQ937298 AGENCOURT
6	847.2	26.0	915	5	BX397020 BX397020
7	840.2	25.8	908	5	BQ716774 AGENCOURT
8	837.8	25.7	918	5	BX326279 BX326279
9	810.6	24.9	901	5	BQ220195 AGENCOURT
10	807.8	24.8	926	5	BX348287 BX348287
11	801.6	24.6	924	4	BII18034 602867301
12	799.2	24.5	1046	5	BQ277739 AGENCOURT
13	797.2	24.5	840	5	BUS57215 AGENCOURT
14	792.2	24.3	820	5	BUB49866 AGENCOURT
15	792.2	24.3	863	5	BUS57274 AGENCOURT
16	781.0	24.0	1027	4	BM476862 AGENCOURT
17	779.6	23.9	907	5	BUS41549 AGENCOURT
18	769.4	23.6	922	5	BUB44769 AGENCOURT
19	767.4	23.6	878	4	BG67934 602633549
20	758.4	23.3	928	5	BUI51020 AGENCOURT
21	755.4	23.2	767	5	BM977746 UI-CF-EN1
22	746.2	22.9	763	5	BM975016 UI-CF-EC1
23	746	22.9	990	2	BE799964
24	743.6	22.8	793	6	CA411919 UI-H-E20-

Page 1

Scoring table:	IDENTITY_NUC	20	378.4	11.6	176940	10	AC132331
Gapop 10.0 , Gapext 1.0		21	378.2	11.6	1980	5	BC075754
Searched:	4526729 seqs, 23644849745 residues	22	338.2	10.4	2348	5	BC063736
Total number of hits satisfying chosen parameters:		9053458					AC132331 Mus muscu
Minimum DB seq length:	0	23	307	9.4	313	6	XNopos 1
Maximum DB seq length:	2000000000	24	234.2	7.2	2048	9	AX341683 Sequence
Post-processing:	Minimum Match 0%	25	234.2	7.2	2818	9	BC002977 Homo sapi
	Maximum Match 100%	26	230.6	7.1	624	9	AK025165 Homo sapi
Database :	GenEmbl:	27	230.6	7.1	1980	9	CR536593 Homo sapi
		28	229	7.0	621	9	SS3268 Homo sapi
		29	229	7.0	624	9	CR542274 Homo sapi
		30	229	7.0	624	9	AF498943 Homo sapi
		31	229	7.0	624	12	BT007184 Homo sapi
		32	229	7.0	660	9	BT008475 Synthetic
		33	229	7.0	1971	6	X56741 H.sapiens m
		34	227.4	7.0	638	10	CQ725816 Sequence
		35	225.4	6.9	1400	10	SS3270 MEI=RAS-rel
		36	224.2	6.9	1337	10	BC071176 Rattus no
		37	222.6	6.8	760	4	XG1990 Mus muscu
		38	222	6.8	1018	5	XG6385 Canine rab8
		39	221.4	6.8	563	5	BX930100 Gallus ga
		40	218.2	6.7	765	5	DXGORA2
		41	217.8	6.7	624	6	AX236078 Sequence
		42	217.8	6.7	1128	9	BC02054 Homo sapi
		43	217.8	6.7	1161	6	AX236076 Sequence
		44	217.8	6.7	1265	9	AB038935 Homo sapi
		45	217.8	6.7	1266	6	CQ725816 Sequence
ALIGNMENTS							
RESULT	1	BC040679					
LOCUS			3326 bp	mRNA			
DEFINITION			Homo sapiens RAB15, member RAS oncogene family, mRNA (cDNA clone MGC:42319 IMAGE:4817835), complete cds.				
ACCESSION		BC040679					
VERSION		BC040679.2					
KEYWORDS			GI:34783346				
SOURCE			MGC.				
ORGANISM			Homo sapiens (human)				
REFERENCE			Homo sapiens				
AUTHORS			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
			1 (bases 1 to 3326)				
			Strausberg, R.D., Feingold, E.A., Grouse, L.H., Derge, J.G., Shemesh, I.M., Schuler, G.D., Altschul, S.F., Zeeberg, B.R., Buetow, K.H., Schaefer, C.F., Blatt, N.K., Hopkins, R.F., Jordan, R., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mulilahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalobos, D.K., Mutzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A., Faley, J., Heitton, B., Ketteman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnurch, A., Schain, J.B., Jones, S.J., and Marra, M.A., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL			Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
PUBMED			1247932				
REFERENCE			2 (bases 1 to 3326)				
AUTHORS			Strausberg, R.				
TITLE			Direct Submission				
JOURNAL			Submitted (29-NOV-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
Result No.	Query Match	Length	DB ID	Description			
1	3030.2	93.0	3326	9 BC040679 Homo sapi			
	2696.6	82.8	190517	AL1302 Human chr			
	1423.8	43.7	2210	BX648025 Homo sapi			
	1192.8	36.6	7924	AX34040 Sequence			
c	1192.8	36.6	7924	AX348456 Sequence			
c	1160.8	35.6	7924	AX347041 Sequence			
c	1160.8	35.6	7924	AX348457 Sequence			
	1000.2	30.7	1054	AX39903 Sequence			
	866.2	26.6	895	BD205055 Human nuc			
	866.2	26.6	895	AX014147 Sequence			
	813.2	25.0	3139	BC027769 Mus muscu			
	633.9	19.4	676	AX781147 Sequence			
	577.6	17.7	945	M83779 Sprague-Daw			
	496.1	15.2	579	CQ730386 Sequence			
	477.4	14.7	481	AX396088 Sequence			
c	438.8	13.5	463	AX334820 Sequence			
c	423.6	13.0	270654	AC096084 Rattus no			
	416.4	12.8	2560	BC013790 Mus muscu			
	383.9	11.8	410	AX779778 Sequence			

